

SEQUENCE LISTING

<110> DNAVEC RESEARCH INC.

<120> Method of Treating Inflammatory Disease
Associated With Bone Destruction

<130> D3-A0206P

<150> JP 2003-075964

<151> 2003-03-19

<160> 6

<170> PatentIn version 3.1

<210> 1

<211> 900

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(900)

<223>

<400> 1

atg tgg agc tgg aag tgc ctc ctc ttc tgg gct gtg ctg gtc aca gcc 48
Met Trp Ser Trp Lys Cys Leu Leu Phe Trp Ala Val Leu Val Thr Ala
1 5 10 15

aca ctc tgc acc gct agg ccg tcc ccg acc ttg cct gaa caa gat gct 96
Thr Leu Cys Thr Ala Arg Pro Ser Pro Thr Leu Pro Glu Gln Asp Ala
20 25 30

ctc ccc tcc tcg gag gat gat gat gat gat gac tcc tct tca gag 144
Leu Pro Ser Ser Glu Asp Asp Asp Asp Asp Asp Ser Ser Ser Glu
35 40 45

gag aaa gaa aca gat aac acc aaa cca aac ccc gta gct cca tat tgg 192
Glu Lys Glu Thr Asp Asn Thr Lys Pro Asn Pro Val Ala Pro Tyr Trp
50 55 60

aca tcc cca gaa aag atg gaa aag aaa ttg cat gca gtg ccg gct gcc	240
Thr Ser Pro Glu Lys Met Glu Lys Lys Leu His Ala Val Pro Ala Ala	
65 70 75 80	
aag aca gtg aag ttc aaa tgc cct tcc agt ggg acc cca aac ccc aca	288
Lys Thr Val Lys Phe Lys Cys Pro Ser Ser Gly Thr Pro Asn Pro Thr	
85 90 95	
ctg cgc tgg ttg aaa aat ggc aaa gaa ttc aaa cct gac cac aga att	336
Leu Arg Trp Leu Lys Asn Gly Lys Glu Phe Lys Pro Asp His Arg Ile	
100 105 110	
gga ggc tac aag gtc cgt tat gcc acc tgg agc atc ata atg gac tct	384
Gly Gly Tyr Lys Val Arg Tyr Ala Thr Trp Ser Ile Ile Met Asp Ser	
115 120 125	
gtg gtg ccc tct gac aag ggc aac tac acc tgc att gtg gag aat gag	432
Val Val Pro Ser Asp Lys Gly Asn Tyr Thr Cys Ile Val Glu Asn Glu	
130 135 140	
tac ggc agc atc aac cac aca tac cag ctg gat gtc gtg gag cgg tcc	480
Tyr Gly Ser Ile Asn His Thr Tyr Gln Leu Asp Val Val Glu Arg Ser	
145 150 155 160	
cct cac cgg ccc atc ctg caa gca ggg ttg ccc gcc aac aaa aca gtg	528
Pro His Arg Pro Ile Leu Gln Ala Gly Leu Pro Ala Asn Lys Thr Val	
165 170 175	
gcc ctg ggt agc aac gtg gag ttc atg tgt aag gtg tac agt gac ccg	576
Ala Leu Gly Ser Asn Val Glu Phe Met Cys Lys Val Tyr Ser Asp Pro	
180 185 190	
cag ccg cac atc cag tgg cta aag cac atc gag gtg aat ggg agc aag	624
Gln Pro His Ile Gln Trp Leu Lys His Ile Glu Val Asn Gly Ser Lys	
195 200 205	
att ggc cca gac aac ctg cct tat gtc cag atc ttg aag gta atc atg	672
Ile Gly Pro Asp Asn Leu Pro Tyr Val Gln Ile Leu Lys Val Ile Met	
210 215 220	
gca cca gtc ttc gtg ggc cag tct act ggg aag gag acc act gtc tgc	720

Ala Pro Val Phe Val Gly Gln Ser Thr Gly Lys Glu Thr Thr Val Ser
 225 230 235 240

ggg gct caa gtt cct gtg ggc agg ctc agt tgc ccc cga atg gga tca 768
 Gly Ala Gln Val Pro Val Gly Arg Leu Ser Cys Pro Arg Met Gly Ser
 245 250 255

ttc ctc acg ctt cag gca cac aca ctc cat ctc agt agg gat cta gcc 816
 Phe Leu Thr Leu Gln Ala His Thr Leu His Leu Ser Arg Asp Leu Ala
 260 265 270

aca tcc ccc agg act agt aac aga ggt cac aaa gtg gag gtg agc tgg 864
 Thr Ser Pro Arg Thr Ser Asn Arg Gly His Lys Val Glu Val Ser Trp
 275 280 285

gaa cag agg gct gca ggg atg ggt ggt gct ggt ctg 900
 Glu Gln Arg Ala Ala Gly Met Gly Gly Ala Gly Leu
 290 295 300

<210> 2
 <211> 300
 <212> PRT
 <213> Homo sapiens

<400> 2

Met Trp Ser Trp Lys Cys Leu Leu Phe Trp Ala Val Leu Val Thr Ala
 1 5 10 15

Thr Leu Cys Thr Ala Arg Pro Ser Pro Thr Leu Pro Glu Gln Asp Ala
 20 25 30

Leu Pro Ser Ser Glu Asp Asp Asp Asp Asp Asp Ser Ser Ser Glu
 35 40 45

Glu Lys Glu Thr Asp Asn Thr Lys Pro Asn Pro Val Ala Pro Tyr Trp
 50 55 60

Thr Ser Pro Glu Lys Met Glu Lys Lys Leu His Ala Val Pro Ala Ala
 65 70 75 80

Lys Thr Val Lys Phe Lys Cys Pro Ser Ser Gly Thr Pro Asn Pro Thr

				85					90					95			
Leu	Arg	Trp	Leu	Lys	Asn	Gly	Lys	Glu	Phe	Lys	Pro	Asp	His	Arg	Ile		
			100					105						110			
Gly	Gly	Tyr	Lys	Val	Arg	Tyr	Ala	Thr	Trp	Ser	Ile	Ile	Met	Asp	Ser		
		115					120						125				
Val	Val	Pro	Ser	Asp	Lys	Gly	Asn	Tyr	Thr	Cys	Ile	Val	Glu	Asn	Glu		
		130				135					140						
Tyr	Gly	Ser	Ile	Asn	His	Thr	Tyr	Gln	Leu	Asp	Val	Val	Glu	Arg	Ser		
145					150					155					160		
Pro	His	Arg	Pro	Ile	Leu	Gln	Ala	Gly	Leu	Pro	Ala	Asn	Lys	Thr	Val		
				165					170						175		
Ala	Leu	Gly	Ser	Asn	Val	Glu	Phe	Met	Cys	Lys	Val	Tyr	Ser	Asp	Pro		
			180					185						190			
Gln	Pro	His	Ile	Gln	Trp	Leu	Lys	His	Ile	Glu	Val	Asn	Gly	Ser	Lys		
		195					200						205				
Ile	Gly	Pro	Asp	Asn	Leu	Pro	Tyr	Val	Gln	Ile	Leu	Lys	Val	Ile	Met		
	210					215					220						
Ala	Pro	Val	Phe	Val	Gly	Gln	Ser	Thr	Gly	Lys	Glu	Thr	Thr	Val	Ser		
225					230					235					240		
Gly	Ala	Gln	Val	Pro	Val	Gly	Arg	Leu	Ser	Cys	Pro	Arg	Met	Gly	Ser		
				245					250					255			
Phe	Leu	Thr	Leu	Gln	Ala	His	Thr	Leu	His	Leu	Ser	Arg	Asp	Leu	Ala		
			260					265						270			
Thr	Ser	Pro	Arg	Thr	Ser	Asn	Arg	Gly	His	Lys	Val	Glu	Val	Ser	Trp		
		275					280					285					
Glu	Gln	Arg	Ala	Ala	Gly	Met	Gly	Gly	Ala	Gly	Leu						
	290					295					300						

<210>	3
<211>	945
<212>	DNA
<213>	Homo sapiens

```
<220>
<221> CDS
<222> (1)..(945)
<223>
```

<400>	3
atg gag gcc aga gct cag agt ggc aac ggg tcg cag ccc ttg ctg cag Met Glu Ala Arg Ala Gln Ser Gly Asn Gly Ser Gln Pro Leu Leu Gln	48
1 5 10 15	
acg ccc cgt gac ggt ggc aga cag cg t ggg gag ccc gac ccc aga gac Thr Pro Arg Asp Gly Gly Arg Gln Arg Gly Gl u Pro Asp Pro Arg Asp	96
20 25 30	
gcc ctc acc cag cag gta cat gtc ttg tct ctg gat cag atc aga gcc Ala Leu Thr Gln Gln Val His Val Leu Ser Leu Asp Gln Ile Arg Ala	144
35 40 45	
atc cga aac accaat gag tacaca gag ggg cct act gtc gtc cca aga Ile Arg Asn Thr Asn Gl u Tyr Thr Gl u Gly Pro Thr Val Val Pro Arg	192
50 55 60	
cct ggg ctc aag cct gct cct cgc cc c tcc act cag cac aaa cac gag Pro Gly Leu Lys Pro Ala Pro Arg Pro Ser Thr Gln His Lys His Gl u	240
65 70 75 80	
aga ctc cac ggt ctg cct gag cac cgc cag cct cct agg ctc cag cac Arg Leu His Gly Leu Pro Gl u His Arg Gln Pro Pro Arg Leu Gln His	288
85 90 95	
tcg cag gtc cat tct tct gca cga gcc cct ctg tcc aga tcc ata agc Ser Gln Val His Ser Ser Ala Arg Ala Pro Leu Ser Arg Ser Ile Ser	336
100 105 110	
acg gtc agc tca ggg tcg cgg agc agt acgagg acaagtacc agc agc Thr Val Ser Ser Gly Ser Arg Ser Ser Thr Arg Thr Ser Thr Ser Ser	384
115 120 125	

agc tcc tct gaa cag aga ctg cta gga tca tcc ttc tcc tcc ggg cct	432
Ser Ser Ser Glu Gln Arg Leu Leu Gly Ser Ser Phe Ser Ser Gly Pro	
130 135 140	
gtt gct gat ggc ata atc cgg gtg caa ccc aaa tct gag ctc aag cca	480
Val Ala Asp Gly Ile Ile Arg Val Gln Pro Lys Ser Glu Leu Lys Pro	
145 150 155 160	
ggt gag ctt aag cca ctg agc aag gaa gat ttg ggc ctg cac gcc tac	528
Gly Glu Leu Lys Pro Leu Ser Lys Glu Asp Leu Gly Leu His Ala Tyr	
165 170 175	
agg tgt gag gac tgt ggc aag tgc aaa tgt aag gag tgc acc tac cca	576
Arg Cys Glu Asp Cys Gly Lys Cys Lys Cys Lys Glu Cys Thr Tyr Pro	
180 185 190	
agg cct ctg cca tca gac tgg atc tgc gac aag cag tgc ctt tgc tcg	624
Arg Pro Leu Pro Ser Asp Trp Ile Cys Asp Lys Gln Cys Leu Cys Ser	
195 200 205	
gcc cag aac gtg att gac tat ggg act tgt gta tgc tgt gtg aaa ggt	672
Ala Gln Asn Val Ile Asp Tyr Gly Thr Cys Val Cys Cys Val Lys Gly	
210 215 220	
ctc ttc tat cac tgt tct aat gat gat gag gac aac tgt gct gac aac	720
Leu Phe Tyr His Cys Ser Asn Asp Asp Glu Asp Asn Cys Ala Asp Asn	
225 230 235 240	
cca tgt tct tgc agc cag tct cac tgt tgt aca cga tgg tca gcc atg	768
Pro Cys Ser Cys Ser Gln Ser His Cys Cys Thr Arg Trp Ser Ala Met	
245 250 255	
ggt gtc atg tcc ctc ttt ttg cct tgt tta tgg tgt tac ctt cca gcc	816
Gly Val Met Ser Leu Phe Leu Pro Cys Leu Trp Cys Tyr Leu Pro Ala	
260 265 270	
aag ggt tgc ctt aaa ttg tgc cag ggg tgt tat gac cgg gtt aac agg	864
Lys Gly Cys Leu Lys Leu Cys Gln Gly Cys Tyr Asp Arg Val Asn Arg	
275 280 285	
cct ggt tgc cgc tgt aaa aac tca aac aca gtt tgc tgc aaa gtt ccc	912

Pro Gly Cys Arg Cys Lys Asn Ser Asn Thr Val Cys Cys Lys Val Pro
 290 295 300

act gtc ccc cct agg aac ttt gaa aaa cca aca
 Thr Val Pro Pro Arg Asn Phe Glu Lys Pro Thr
 305 310 315

945

<210> 4
 <211> 315
 <212> PRT
 <213> Homo sapiens

<400> 4

Met Glu Ala Arg Ala Gln Ser Gly Asn Gly Ser Gln Pro Leu Leu Gln
 1 5 10 15

Thr Pro Arg Asp Gly Gly Arg Gln Arg Gly Glu Pro Asp Pro Arg Asp
 20 25 30

Ala Leu Thr Gln Gln Val His Val Leu Ser Leu Asp Gln Ile Arg Ala
 35 40 45

Ile Arg Asn Thr Asn Glu Tyr Thr Glu Gly Pro Thr Val Val Pro Arg
 50 55 60

Pro Gly Leu Lys Pro Ala Pro Arg Pro Ser Thr Gln His Lys His Glu
 65 70 75 80

Arg Leu His Gly Leu Pro Glu His Arg Gln Pro Pro Arg Leu Gln His
 85 90 95

Ser Gln Val His Ser Ser Ala Arg Ala Pro Leu Ser Arg Ser Ile Ser
 100 105 110

Thr Val Ser Ser Gly Ser Arg Ser Ser Thr Arg Thr Ser Thr Ser Ser
 115 120 125

Ser Ser Ser Glu Gln Arg Leu Leu Gly Ser Ser Phe Ser Ser Gly Pro
 130 135 140

Val Ala Asp Gly Ile Ile Arg Val Gln Pro Lys Ser Glu Leu Lys Pro
145 150 155 160

Gly Glu Leu Lys Pro Leu Ser Lys Glu Asp Leu Gly Leu His Ala Tyr
165 170 175

Arg Cys Glu Asp Cys Gly Lys Cys Lys Cys Lys Glu Cys Thr Tyr Pro
180 185 190

Arg Pro Leu Pro Ser Asp Trp Ile Cys Asp Lys Gln Cys Leu Cys Ser
195 200 205

Ala Gln Asn Val Ile Asp Tyr Gly Thr Cys Val Cys Cys Val Lys Gly
210 215 220

Leu Phe Tyr His Cys Ser Asn Asp Asp Glu Asp Asn Cys Ala Asp Asn
225 230 235 240

Pro Cys Ser Cys Ser Gln Ser His Cys Cys Thr Arg Trp Ser Ala Met
245 250 255

Gly Val Met Ser Leu Phe Leu Pro Cys Leu Trp Cys Tyr Leu Pro Ala
260 265 270

Lys Gly Cys Leu Lys Leu Cys Gln Gly Cys Tyr Asp Arg Val Asn Arg
275 280 285

Pro Gly Cys Arg Cys Lys Asn Ser Asn Thr Val Cys Cys Lys Val Pro
290 295 300

Thr Val Pro Pro Arg Asn Phe Glu Lys Pro Thr
305 310 315

<210> 5

<211> 1230

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(1230)

<223>

<400> 5

atg acc gaa gaa aca cac ccg gac gat gac agc tat att gtg cgt gtc	48
Met Thr Glu Glu Thr His Pro Asp Asp Asp Ser Tyr Ile Val Arg Val	
1 5 10 15	

aag gct gtg gtt atg acc aga gat gac tcc agc ggg gga tgg ttc cca	96
Lys Ala Val Val Met Thr Arg Asp Asp Ser Ser Gly Gly Trp Phe Pro	
20 25 30	

cag gaa gga ggc ggg atc agt cgc gtc ggc gtg tgt aag gtc atg cac	144
Gln Glu Gly Gly Gly Ile Ser Arg Val Gly Val Cys Lys Val Met His	
35 40 45	

cct gaa ggc aac gga cga agc ggc ttt ctc atc cat ggc gag cga cag	192
Pro Glu Gly Asn Gly Arg Ser Gly Phe Leu Ile His Gly Glu Arg Gln	
50 55 60	

aaa gac aaa ctg gtg gta ttg gaa tgc tat gtc aga aag gac ttg gtc	240
Lys Asp Lys Leu Val Val Leu Glu Cys Tyr Val Arg Lys Asp Leu Val	
65 70 75 80	

tac acc aaa gcc aat ccg acg ttt cat cat tgg aag gtt gat aac agg	288
Tyr Thr Lys Ala Asn Pro Thr Phe His His Trp Lys Val Asp Asn Arg	
85 90 95	

aag ttt gga ctt act ttc caa agt cct gca gat gca cga gcc ttt gac	336
Lys Phe Gly Leu Thr Phe Gln Ser Pro Ala Asp Ala Arg Ala Phe Asp	
100 105 110	

agg ggc gtg aga aaa gcc att gaa gac ctt ata gaa ggt tca acg acc	384
Arg Gly Val Arg Lys Ala Ile Glu Asp Leu Ile Glu Gly Ser Thr Thr	
115 120 125	

tcc tct tcc act ctc cat aac gaa gct gag ctc gga gac gat gac gtt	432
Ser Ser Ser Thr Leu His Asn Glu Ala Glu Leu Gly Asp Asp Asp Val	
130 135 140	

ttc acg aca gct acg gac agt tct tct aat tcc tcg cag aag agg gag	480
Phe Thr Thr Ala Thr Asp Ser Ser Ser Asn Ser Ser Gln Lys Arg Glu	
145 150 155 160	

ccg act acg agg aca atc tcc tcc ccc acg tcc tgt gag cac cgg aag	528
Pro Thr Thr Arg Thr Ile Ser Ser Pro Thr Ser Cys Glu His Arg Lys	
165 170 175	
att tat acc ctt gac cca tac ccc atg gac cat tac cac cct gac cag	576
Ile Tyr Thr Leu Asp Pro Tyr Pro Met Asp His Tyr His Pro Asp Gln	
180 185 190	
cgg ttg ccg cgg tcc tac ccc cag gtc acc ttc cca gaa gat gat gaa	624
Arg Leu Pro Arg Ser Tyr Pro Gln Val Thr Phe Pro Glu Asp Asp Glu	
195 200 205	
gaa att gta cgc atc aac ccc cga gag aag atc tgg atg acc ggt tat	672
Glu Ile Val Arg Ile Asn Pro Arg Glu Lys Ile Trp Met Thr Gly Tyr	
210 215 220	
gaa gac tac cgg cac gcg ccg gtt cgc ggc aaa tac tta gac acc aca	720
Glu Asp Tyr Arg His Ala Pro Val Arg Gly Lys Tyr Leu Asp Thr Thr	
225 230 235 240	
gaa gac gcg gac tcc tac gtg cgc ttc gcc aag ggc gaa gtc ccc aaa	768
Glu Asp Ala Asp Ser Tyr Val Arg Phe Ala Lys Gly Glu Val Pro Lys	
245 250 255	
cac gaa tat acc tat ccc tat gtt gat tct tcg gac ttc ggc ttc ggg	816
His Glu Tyr Thr Tyr Pro Tyr Val Asp Ser Ser Asp Phe Gly Phe Gly	
260 265 270	
gag gat ccc aaa ggt agt gtg atc aag aca cag ccg ccc agg gcc aag	864
Glu Asp Pro Lys Gly Ser Val Ile Lys Thr Gln Pro Pro Arg Ala Lys	
275 280 285	
tcc cgt cgg cgg aag gag aac ggc gaa cgg tcg cgg tgt gtg tac tgc	912
Ser Arg Arg Arg Lys Glu Asn Gly Glu Arg Ser Arg Cys Val Tyr Cys	
290 295 300	
agg gat atg ttt aat cac gaa gag aac cga agg ggc cac tgc caa gac	960
Arg Asp Met Phe Asn His Glu Glu Asn Arg Arg Gly His Cys Gln Asp	
305 310 315 320	
gcg ccc gac gcc gtg aga act tgc att cgc cgg gtg agc tgt atg tgg	1008

Ala Pro Asp Ala Val Arg Thr Cys Ile Arg Arg Val Ser Cys Met Trp
 325 330 335

tgc gcg gac agc atg ctg tac cac tgt atg tcc gac ccc gag gga gac 1056
 Cys Ala Asp Ser Met Leu Tyr His Cys Met Ser Asp Pro Glu Gly Asp
 340 345 350

tac act gac cct tgt tcg tgt gac aca agc gat gag aag ttt tgc ctc 1104
 Tyr Thr Asp Pro Cys Ser Cys Asp Thr Ser Asp Glu Lys Phe Cys Leu
 355 360 365

cgg tgg atg gct cta att gcc ttg tct ttc ctg gcc cct tgt atg tgc 1152
 Arg Trp Met Ala Leu Ile Ala Leu Ser Phe Leu Ala Pro Cys Met Cys
 370 375 380

tgt tac ctg ccc ctc cgg gcc tgc cac cgc tgt gga gtg atg tgc agg 1200
 Cys Tyr Leu Pro Leu Arg Ala Cys His Arg Cys Gly Val Met Cys Arg
 385 390 395 400

tgc tgt ggt ggg aag cac aaa gcc gcc gcg 1230
 Cys Cys Gly Gly Lys His Lys Ala Ala Ala
 405 410

<210> 6
 <211> 410
 <212> PRT
 <213> Mus musculus

<400> 6

Met Thr Glu Glu Thr His Pro Asp Asp Asp Ser Tyr Ile Val Arg Val
 1 5 10 15

Lys Ala Val Val Met Thr Arg Asp Asp Ser Ser Gly Gly Trp Phe Pro
 20 25 30

Gln Glu Gly Gly Gly Ile Ser Arg Val Gly Val Cys Lys Val Met His
 35 40 45

Pro Glu Gly Asn Gly Arg Ser Gly Phe Leu Ile His Gly Glu Arg Gln
 50 55 60

Lys	Asp	Lys	Leu	Val	Val	Leu	Glu	Cys	Tyr	Val	Arg	Lys	Asp	Leu	Val	65	70	75	80
Tyr	Thr	Lys	Ala	Asn	Pro	Thr	Phe	His	His	Trp	Lys	Val	Asp	Asn	Arg	85	90	95	
Lys	Phe	Gly	Leu	Thr	Phe	Gln	Ser	Pro	Ala	Asp	Ala	Arg	Ala	Phe	Asp	100	105	110	
Arg	Gly	Val	Arg	Lys	Ala	Ile	Glu	Asp	Leu	Ile	Glu	Gly	Ser	Thr	Thr	115	120	125	
Ser	Ser	Ser	Thr	Leu	His	Asn	Glu	Ala	Glu	Leu	Gly	Asp	Asp	Asp	Val	130	135	140	
Phe	Thr	Thr	Ala	Thr	Asp	Ser	Ser	Ser	Asn	Ser	Ser	Gln	Lys	Arg	Glu	145	150	155	160
Pro	Thr	Thr	Arg	Thr	Ile	Ser	Ser	Pro	Thr	Ser	Cys	Glu	His	Arg	Lys	165	170	175	
Ile	Tyr	Thr	Leu	Asp	Pro	Tyr	Pro	Met	Asp	His	Tyr	His	Pro	Asp	Gln	180	185	190	
Arg	Leu	Pro	Arg	Ser	Tyr	Pro	Gln	Val	Thr	Phe	Pro	Glu	Asp	Asp	Glu	195	200	205	
Glu	Ile	Val	Arg	Ile	Asn	Pro	Arg	Glu	Lys	Ile	Trp	Met	Thr	Gly	Tyr	210	215	220	
Glu	Asp	Tyr	Arg	His	Ala	Pro	Val	Arg	Gly	Lys	Tyr	Leu	Asp	Thr	Thr	225	230	235	240
Glu	Asp	Ala	Asp	Ser	Tyr	Val	Arg	Phe	Ala	Lys	Gly	Glu	Val	Pro	Lys	245	250	255	
His	Glu	Tyr	Thr	Tyr	Pro	Tyr	Val	Asp	Ser	Ser	Asp	Phe	Gly	Phe	Gly	260	265	270	
Glu	Asp	Pro	Lys	Gly	Ser	Val	Ile	Lys	Thr	Gln	Pro	Pro	Arg	Ala	Lys	275	280	285	

Ser Arg Arg Arg Lys Glu Asn Gly Glu Arg Ser Arg Cys Val Tyr Cys
 290 295 300

Arg Asp Met Phe Asn His Glu Glu Asn Arg Arg Gly His Cys Gln Asp
 305 310 315 320

Ala Pro Asp Ala Val Arg Thr Cys Ile Arg Arg Val Ser Cys Met Trp
 325 330 335

Cys Ala Asp Ser Met Leu Tyr His Cys Met Ser Asp Pro Glu Gly Asp
 340 345 350

Tyr Thr Asp Pro Cys Ser Cys Asp Thr Ser Asp Glu Lys Phe Cys Leu
 355 360 365

Arg Trp Met Ala Leu Ile Ala Leu Ser Phe Leu Ala Pro Cys Met Cys
 370 375 380

Cys Tyr Leu Pro Leu Arg Ala Cys His Arg Cys Gly Val Met Cys Arg
 385 390 395 400

Cys Cys Gly Gly Lys His Lys Ala Ala Ala
 405 410